

## CRF Errors Corrected by the STIC Systems Branch

SU40

OIP

Serial Number: 10/088,0

CRF Processing Date: 4/4/02

Edited by:

Verified by:

(STIC staff)

 Changed a file from non-ASCII to ASCII Changed the margins in cases where the sequence text was "wrapped" down to the next line Edited a format error in the Current Application Data section, specifically: Edited the Current Application Data section with the actual current number. The number inputted by the applicant was  the prior application data; or  other \_\_\_\_\_. Added the mandatory heading and subheadings for "Current Application Data". Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer. Changed the spelling of a mandatory field (the headings or subheadings), specifically: Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place. Inserted colons after headings/subheadings. Headings edited included: Deleted extra, invalid, headings used by an applicant, specifically: Deleted:  non-ASCII "garbage" at the beginning/end of files;  secretary initials/filename at end of file;  page numbers throughout text;  other invalid text, such as "primer" in Seq ID 5 in the <213> field Inserted mandatory headings, specifically: Corrected an obvious error in the response, specifically: Edited identifiers where upper case is used but lower case is required, or vice versa. Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: Other:

ENTERED #5

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



Does Not Comply      OIPE  
Corrected Dictation Needed  
Entered on p. 5

Errors on p. 5

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/088,045

DATE: 04/04/2002  
TIME: 15:17:37

Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\04042002\J088045.raw

4 <110> APPLICANT: Joelle Thonnard  
6 <120> TITLE OF INVENTION: Novel Compounds  
9 <130> FILE REFERENCE: BM45412  
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/088,045  
C--> 11 <141> CURRENT FILING DATE: 2002-03-14  
11 <150> PRIOR APPLICATION NUMBER: 9921691.3  
12 <151> PRIOR FILING DATE: 1999-09-14  
14 <160> NUMBER OF SEQ ID NOS: 10  
16 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
18 <210> SEQ ID NO: 1  
19 <211> LENGTH: 1509  
20 <212> TYPE: DNA  
21 <213> ORGANISM: Moraxella catarrhalis  
23 <400> SEQUENCE: 1  
24 atgtctaagg ctactttgat aaaaaacaacc ttaattttgtg ccttaagtgc attgatgctc 60  
25 agtgggttgc gcaatcaagg ggacaaagcc gcccagccaa aaagcagcac ggttagacgct 120  
26 gccgccaaga cagcaaatgc agataatgct gcctcacaag aacatcaagg cgagctgcct 180  
27 gtcattgtat ccattgttac gcatgcacca gaagttccac cacctgttga ccgtgaccac 240  
28 cccgccaagg tgggtgtaaa aatgaaaacc gttgaaaaag tcattgcgtct ggcagatggc 300  
29 gtggaaatatc agttttggac atttggcggt caagttccag ggcagatgtat tcgtgtgcgt 360  
30 gaaggcgaca ccatcgaagt gcagttctca aaccaccagg attcaaaaat gccccataat 420  
31 gttgactttc acgctgccc acggcctggc ggcggggcag aagcgtcatt taccgcaccc 480  
32 ggtcatacat caacctttag tttaaagcc ttacagcctg gttgttatgt ctatcactgt 540  
33 gcgggttgc cttgtggcat gcacattgtt aatggcatgt atggtttgtat tttgggtgaa 600  
34 ccaaaagagg gcttgccaaa agtagataaa gaataactatg tcattgcagg cgactttat 660  
35 accaaaggca aatatggcga acaaggctca cagcccttgc atatggaaaa agccattcga 720  
36 gaagatgctg aatatgttgc tttaatggc tggtggggg cggtgactgg tgaaaatgtc 780  
37 ctaaaagcca aggttggcga aactgttcgc ttattttgtgg gtaacggcgg cccgaatttg 840  
38 acatcatcat tccatgtcat tggtgagatt ttgtataagg ttcaatttgc ggggtgtaa 900  
39 ggtgaaaacc acaatatc aaccacgcta atcccagcag gtggcgctgc catcaactgaa 960  
40 tttaaggtgg atgtgccggg tgattatgtc ttgggtgacc atgcccattt ccgtgcctt 1020  
41 aacaaagggg cattgggcat acttaagggtg gaaggtgaag aaaatcatga gatttattca 1080  
42 cacaaacaaa cagacgctgt ctatcgttca gagggtgccc cacaaggcaat tgataaccaa 1140  
43 gaagcaccca aaacacctgc acctgccaac ttacaagagc agattaaagc aggtaaaggca 1200  
44 acctatgact ctaactgtgc tgcttgcac caacctgtat gtaaaggcgt gccaaacgct 1260  
45 ttcccaccgc ttgccaactc tgactatctg aacgcccacc acgctcgtgc cgccagcatc 1320  
46 gtggcaaattt gattgtctgg taagattacc gtcaatgca accaatatgt aagcgtcatg 1380  
47 cctgcgattt ctctgagcga ccaacagatt gccaatgtca tcacccatcac gcttaacagc 1440  
48 tttggtaaca aaggcggcactca actcgtgca gacgatgtgg caaaaagccaa aaaaacccaag 1500  
49 ccaaaactgt 1509  
51 <210> SEQ ID NO: 2  
52 <211> LENGTH: 502  
53 <212> TYPE: PRT

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54 <213> ORGANISM: Moraxella catarrhalis  
56 <400> SEQUENCE: 2  
57 Met Ser Lys Pro Thr Leu Ile Lys Thr Thr Leu Ile Cys Ala Leu Ser  
58 1 5 10 15  
59 Ala Leu Met Leu Ser Gly Cys Ser Asn Gln Ala Asp Lys Ala Ala Gln  
60 20 25 30  
61 Pro Lys Ser Ser Thr Val Asp Ala Ala Lys Thr Ala Asn Ala Asp  
62 35 40 45  
63 Asn Ala Ala Ser Gln Glu His Gln Gly Glu Leu Pro Val Ile Asp Ala  
64 50 55 60  
65 Ile Val Thr His Ala Pro Glu Val Pro Pro Val Asp Arg Asp His  
66 65 70 75 80  
67 Pro Ala Lys Val Val Val Lys Met Glu Thr Val Glu Lys Val Met Arg  
68 85 90 95  
69 Leu Ala Asp Gly Val Glu Tyr Gln Phe Trp Thr Phe Gly Gly Gln Val  
70 100 105 110  
71 Pro Gly Gln Met Ile Arg Val Arg Glu Gly Asp Thr Ile Glu Val Gln  
72 115 120 125  
73 Phe Ser Asn His Pro Asp Ser Lys Met Pro His Asn Val Asp Phe His  
74 130 135 140  
75 Ala Ala Thr Gly Pro Gly Gly Ala Glu Ala Ser Phe Thr Ala Pro  
76 145 150 155 160  
77 Gly His Thr Ser Thr Phe Ser Phe Lys Ala Leu Gln Pro Gly Leu Tyr  
78 165 170 175  
79 Val Tyr His Cys Ala Val Ala Pro Val Gly Met His Ile Ala Asn Gly  
80 180 185 190  
81 Met Tyr Gly Leu Ile Leu Val Glu Pro Lys Glu Gly Leu Pro Lys Val  
82 195 200 205  
83 Asp Lys Glu Tyr Tyr Val Met Gln Gly Asp Phe Tyr Thr Lys Gly Lys  
84 210 215 220  
85 Tyr Gly Glu Gln Gly Leu Gln Pro Phe Asp Met Glu Lys Ala Ile Arg  
86 225 230 235 240  
87 Glu Asp Ala Glu Tyr Val Val Phe Asn Gly Ser Val Gly Ala Leu Thr  
88 245 250 255  
89 Gly Glu Asn Ala Leu Lys Ala Lys Val Gly Glu Thr Val Arg Leu Phe  
90 260 265 270  
91 Val Gly Asn Gly Pro Asn Leu Thr Ser Ser Phe His Val Ile Gly  
92 275 280 285  
93 Glu Ile Phe Asp Lys Val His Phe Glu Gly Gly Lys Gly Glu Asn His  
94 290 295 300  
95 Asn Ile Gln Thr Thr Leu Ile Pro Ala Gly Gly Ala Ala Ile Thr Glu  
96 305 310 315 320  
97 Phe Lys Val Asp Val Pro Gly Asp Tyr Val Leu Val Asp His Ala Ile  
98 325 330 335  
99 Phe Arg Ala Phe Asn Lys Gly Ala Leu Gly Ile Leu Lys Val Glu Gly  
100 340 345 350  
101 Glu Glu Asn His Glu Ile Tyr Ser His Lys Gln Thr Asp Ala Val Tyr  
102 355 360 365  
103 Leu Pro Glu Gly Ala Pro Gln Ala Ile Asp Thr Gln Glu Ala Pro Lys

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104	370	375	380	
105	Thr Pro Ala Pro Ala Asn Leu Gln Glu Gln Ile Lys Ala Gly Lys Ala			
106	385	390	395	400
107	Thr Tyr Asp Ser Asn Cys Ala Ala Cys His Gln Pro Asp Gly Lys Gly			
108	405	410	415	
109	Val Pro Asn Ala Phe Pro Pro Leu Ala Asn Ser Asp Tyr Leu Asn Ala			
110	420	425	430	
111	Asp His Ala Arg Ala Ala Ser Ile Val Ala Asn Gly Leu Ser Gly Lys			
112	435	440	445	
113	Ile Thr Val Asn Gly Asn Gln Tyr Glu Ser Val Met Pro Ala Ile Ala			
114	450	455	460	
115	Leu Ser Asp Gln Gln Ile Ala Asn Val Ile Thr Tyr Thr Leu Asn Ser			
116	465	470	475	480
117	Phe Gly Asn Lys Gly Gly Gln Leu Ser Ala Asp Asp Val Ala Lys Ala			
118	485	490	495	
119	Lys Lys Thr Lys Pro Asn			
120	500			
122	<210> SEQ ID NO: 3			
123	<211> LENGTH: 1506			
124	<212> TYPE: DNA			
125	<213> ORGANISM: Moraxella catarrhalis			
127	<400> SEQUENCE: 3			
128	atgtctaagc ctactttgat aaaaacaacc ttaatttgc ccttaagtgc attgatgctc	60		
129	agtgggttgc gcaatcaagc ggacaaagcc gcccagccaa aaagcagcac ggttagacgct	120		
130	gccgccaaga cagcaaatgc agataatgt gcctcacaag aacatcaagg cgagctgcct	180		
131	gtcattgtat ccattgttac gcatgaccca gaagttccac cacctgttga ccgtgaccac	240		
132	cccgccaaag tgggtgtaaa aatggaaacc gttgaaaaag tcatgcgtct ggcagatggc	300		
133	gttggatatac agttttggac atttggcggt caagttccag ggcagatgat tcgtgtgcgt	360		
134	gaaggcgaca ccatcgaagt gcagttctca aaccaccccg attcaaaaat gccccataat	420		
135	gttgactttc acgctgccc acggcctggc ggcggggcag aagcgtcatt tacccgaccg	480		
136	ggtcatacat caacccattt tag tttaaagcc ttacagcctg gtttgtatgt ctatcactgt	540		
137	gcgggttgcgc ctgttggcat gcacattgt aatggcatgt atggtttgc tttgggttggaa	600		
138	ccaaaagagg gcttgcacaa agtagataaa gaatactatg tcatgcaagg cgacttttat	660		
139	acccaaaggca aatatggcga acaaggtcta cagcccttgc atatggaaaa agcatttcga	720		
140	gaagatgctg aatatgttgc tttaatggc tcgggtgggg cggtgactgg tgaaaatgct	780		
141	ctaaaagcca aggttggcga aactgttgc ttatttgc gtaacggcgg cccaaatttgc	840		
142	acatcatcat tccatgtcat tggtgagatt tttgataagg ttcaacttgc ggggttggaa	900		
143	ggtaaaaacc acaatatacc aaccacgcta atcccgacg gtggcgctgc catcaactgaa	960		
144	tttaagggttgc atgtggccgg tgattatgtc ttgggttgc gatccatctt ccgtgcctt	1020		
145	acccaaaggccc cattgggcatt acttaagggtt gaaagggttgc aaaaatcatgc gatttattca	1080		
146	cacaaacaaa cagacgctgt ctatctgc gagggttgc cacaagcaat tgataccaa	1140		
147	gaagcaccacca aaacacccatgc acctggccaa ttacaaggac agatcaaaggca aggttggca	1200		
148	acctatgact ctaactgtgc tgcttgcac caacctgtat gtaaaggcggt gccaaacgct	1260		
149	ttcccacccgc ttgccaactc tgactatctg aacggccgacc acgctgtgc cgccagcatc	1320		
150	gtggcaaatg gattgtctgg taagattacc gtcaatggca accaatatgc aagcgatgt	1380		
151	cctcgatgg ctctgagcga ccaacagatt gccaatgtca tcacctacac gcttaacagc	1440		
152	tttggtaaca aaggcggtca actcagtgca gacgatgtgg caaaagccaa aaaaaccaag	1500		
153	ccaaac	1506		
155	<210> SEQ ID NO: 4			

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156 <211> LENGTH: 502  
 157 <212> TYPE: PRT  
 158 <213> ORGANISM: Moraxella catarrhalis  
 160 <400> SEQUENCE: 4  
 161 Met Ser Lys Pro Thr Leu Ile Lys Thr Thr Leu Ile Cys Ala Leu Ser  
 162 1 5 10 15  
 163 Ala Leu Met Leu Ser Gly Cys Ser Asn Gln Ala Asp Lys Ala Ala Gln  
 164 20 25 30  
 165 Pro Lys Ser Ser Thr Val Asp Ala Ala Ala Lys Thr Ala Asn Ala Asp  
 166 35 40 45  
 167 Asn Ala Ala Ser Gln Glu His Gln Gly Glu Leu Pro Val Ile Asp Ala  
 168 50 55 60  
 169 Ile Val Thr His Ala Pro Glu Val Pro Pro Pro Val Asp Arg Asp His  
 170 65 70 75 80  
 171 Pro Ala Lys Val Val Val Lys Met Glu Thr Val Glu Lys Val Met Arg  
 172 85 90 95  
 173 Leu Ala Asp Gly Val Glu Tyr Gln Phe Trp Thr Phe Gly Gly Gln Val  
 174 100 105 110  
 175 Pro Gly Gln Met Ile Arg Val Arg Glu Gly Asp Thr Ile Glu Val Gln  
 176 115 120 125  
 177 Phe Ser Asn His Pro Asp Ser Lys Met Pro His Asn Val Asp Phe His  
 178 130 135 140  
 179 Ala Ala Thr Gly Pro Gly Gly Ala Glu Ala Ser Phe Thr Ala Pro  
 180 145 150 155 160  
 181 Gly His Thr Ser Thr Phe Ser Phe Lys Ala Leu Gln Pro Gly Leu Tyr  
 182 165 170 175  
 183 Val Tyr His Cys Ala Val Ala Pro Val Gly Met His Ile Ala Asn Gly  
 184 180 185 190  
 185 Met Tyr Gly Leu Ile Leu Val Glu Pro Lys Glu Gly Leu Pro Lys Val  
 186 195 200 205  
 187 Asp Lys Glu Tyr Tyr Val Met Gln Gly Asp Phe Tyr Thr Lys Gly Lys  
 188 210 215 220  
 189 Tyr Gly Glu Gln Gly Leu Gln Pro Phe Asp Met Glu Lys Ala Ile Arg  
 190 225 230 235 240  
 191 Glu Asp Ala Glu Tyr Val Val Phe Asn Gly Ser Val Gly Ala Leu Thr  
 192 245 250 255  
 193 Gly Glu Asn Ala Leu Lys Ala Lys Val Gly Glu Thr Val Arg Leu Phe  
 194 260 265 270  
 195 Val Gly Asn Gly Pro Asn Leu Thr Ser Ser Phe His Val Ile Gly  
 196 275 280 285  
 197 Glu Ile Phe Asp Lys Val His Phe Glu Gly Gly Lys Gly Glu Asn His  
 198 290 295 300  
 199 Asn Ile Gln Thr Thr Leu Ile Pro Ala Gly Gly Ala Ala Ile Thr Glu  
 200 305 310 315 320  
 201 Phe Lys Val Asp Val Pro Gly Asp Tyr Val Leu Val Asp His Ala Ile  
 202 325 330 335  
 203 Phe Arg Ala Phe Asn Lys Gly Ala Leu Gly Ile Leu Lys Val Glu Gly  
 204 340 345 350  
 205 Glu Glu Asn His Glu Ile Tyr Ser His Lys Gln Thr Asp Ala Val Tyr

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206 355 360 365  
 207 Leu Pro Glu Gly Ala Pro Gln Ala Ile Asp Thr Gln Glu Ala Pro Lys  
 208 370 375 380  
 209 Thr Pro Ala Pro Ala Asn Leu Gln Glu Gln Ile Lys Ala Gly Lys Ala  
 210 385 390 395 400  
 211 Thr Tyr Asp Ser Asn Cys Ala Ala Cys His Gln Pro Asp Gly Lys Gly  
 212 405 410 415  
 213 Val Pro Asn Ala Phe Pro Pro Leu Ala Asn Ser Asp Tyr Leu Asn Ala  
 214 420 425 430  
 215 Asp His Ala Arg Ala Ala Ser Ile Val Ala Asn Gly Leu Ser Gly Lys  
 216 435 440 445  
 217 Ile Thr Val Asn Gly Asn Gln Tyr Glu Ser Val Met Pro Ala Ile Ala  
 218 450 455 460  
 219 Leu Ser Asp Gln Gln Ile Ala Asn Val Ile Thr Tyr Thr Leu Asn Ser  
 220 465 470 475 480  
 221 Phe Gly Asn Lys Gly Gln Leu Ser Ala Asp Asp Val Ala Lys Ala  
 222 485 490 495  
 223 Lys Lys Thr Lys Pro Asn  
 224 500  
 226 <210> SEQ ID NO: 5  
 227 <211> LENGTH: 21  
 228 <212> TYPE: DNA  
 C--> 229 <213> ORGANISM: *primerArtificial Sequence* *delete*  
 231 <220> FEATURE:  
 232 <223> OTHER INFORMATION: primer  
 234 <400> SEQUENCE: 5  
 235 aaggcgaacag tttcgccaaac c 21  
 237 <210> SEQ ID NO: 6  
 238 <211> LENGTH: 23  
 239 <212> TYPE: DNA  
 240 <213> ORGANISM: Artificial Sequence  
 242 <220> FEATURE:  
 243 <223> OTHER INFORMATION: primer  
 245 <400> SEQUENCE: 6  
 246 gggggcgttt actgggtaaaa atg 23  
 248 <210> SEQ ID NO: 7  
 249 <211> LENGTH: 17  
 250 <212> TYPE: DNA  
 251 <213> ORGANISM: Artificial Sequence  
 253 <220> FEATURE:  
 254 <223> OTHER INFORMATION: primer  
 256 <400> SEQUENCE: 7  
 257 gtaaaacgac ggccagt , 17  
 259 <210> SEQ ID NO: 8  
 260 <211> LENGTH: 17  
 261 <212> TYPE: DNA  
 262 <213> ORGANISM: Artificial Sequence  
 264 <220> FEATURE:  
 265 <223> OTHER INFORMATION: primer

VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/088,045

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:229 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5